Phyre²

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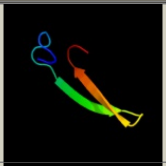
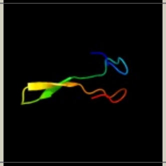
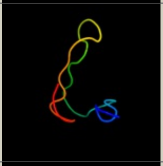
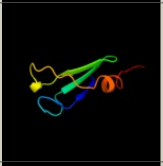
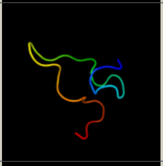
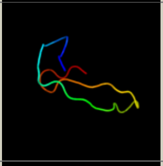
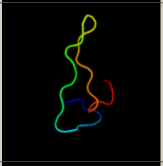
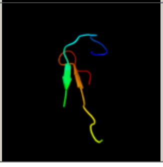
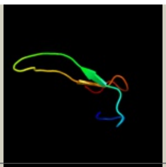
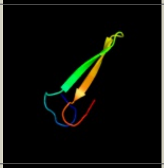
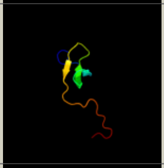
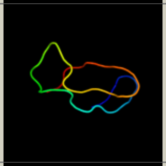
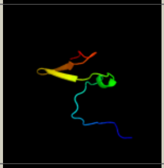
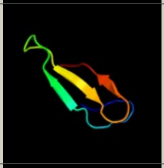
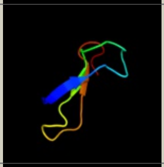
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k81a_	Alignment		90.7	25	**Fold:**Zinc-binding domain of translation initiation factor 2 beta **Superfamily:**Zinc-binding domain of translation initiation factor 2 beta **Family:**Zinc-binding domain of translation initiation factor 2 beta
2	c2e9hA_	Alignment		88.5	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5
3	c3h0gI_	Alignment		88.1	36	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
4	c1neeA_	Alignment		87.9	30	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 beta **PDBTitle:** structure of archaeal translation factor aif2beta from2 methanobacterium thermoautrophicum
5	d1nuia2	Alignment		84.8	20	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
6	c3cw2M_	Alignment		80.6	27	**PDB header:**translation **Chain:** M: **PDB Molecule:**translation initiation factor 2 subunit beta; **PDBTitle:** crystal structure of the intact archaeal translation2 initiation factor 2 from sulfolobus solfataricus .
7	c2dcuB_	Alignment		78.4	23	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation initiation factor 2 beta subunit; **PDBTitle:** crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
8	d1twfi2	Alignment		74.3	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
9	d1qypa_	Alignment		73.6	26	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
10	c3k7aM_	Alignment		71.2	32	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
11	c1y1yS_	Alignment		68.6	23	**PDB header:**transferase/transcription/dna-rna hybrid **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis-dna/rna complex

12	c1pqvS_	Alignment		66.9	23	**PDB header:**transferase/transcription **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis complex
13	d1tfia_	Alignment		65.4	20	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
14	c1i3ql_	Alignment		64.4	20	**PDB header:**transcription **Chain:** l: **PDB Molecule:**dna-directed rna polymerase ii 14.2kd **PDBTitle:** rna polymerase ii crystal form i at 3.1 a resolution
15	c2nn6I_	Alignment		61.4	14	**PDB header:**hydrolase/transferase **Chain:** I: **PDB Molecule:**3'-5' exoribonuclease csl4 homolog; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
16	c2kpiA_	Alignment		60.4	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sco3027; **PDBTitle:** solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
17	c2ba1B_	Alignment		59.9	28	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
18	c2qkdA_	Alignment		57.2	32	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains
19	c1nuiA_	Alignment		55.8	19	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
20	d1wiia_	Alignment		55.4	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
21	d2fiya1	Alignment	not modelled	54.1	28	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
22	c2qa4Z_	Alignment	not modelled	45.6	25	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
23	d2nn6i1	Alignment	not modelled	44.2	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
24	d1jj2y_	Alignment	not modelled	43.6	29	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
25	d1ffkw_	Alignment	not modelled	43.4	29	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
26	d2jnya1	Alignment	not modelled	41.3	9	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
27	c2zkrz_	Alignment	not modelled	41.2	21	**PDB header:**ribosomal protein/rna **Chain:** Z: **PDB Molecule:**e site t-rna; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
28	d1vqoz1	Alignment	not modelled	39.7	25	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
						PDB header:ribosome

29	c3cc4Z_	Alignment	not modelled	39.1	21	**Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** co-crystal structure of anisomycin bound to the 50s ribosomal subunit
30	c2y69S_	Alignment	not modelled	38.6	18	**PDB header:**electron transport **Chain:** S: **PDB Molecule:**cytochrome c oxidase subunit 5b; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
31	c3n9mC_	Alignment	not modelled	38.5	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** cekdm7a from c.elegans, alone
32	c3cngC_	Alignment	not modelled	37.7	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
33	d1pfta_	Alignment	not modelled	35.7	23	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
34	c2x5cB_	Alignment	not modelled	35.6	42	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hypothetical protein orf131; **PDBTitle:** crystal structure of hypothetical protein orf131 from2 pyrobaculum spherical virus
35	d1v54f_	Alignment	not modelled	35.0	17	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Cytochrome c oxidase Subunit F
36	c4a17Y_	Alignment	not modelled	34.8	21	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**rpl37a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
37	c1yshD_	Alignment	not modelled	34.3	21	**PDB header:**structural protein/rna **Chain:** D: **PDB Molecule:**ribosomal protein l37a; **PDBTitle:** localization and dynamic behavior of ribosomal protein l30e
38	d3gata_	Alignment	not modelled	32.0	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
39	d2ct7a1	Alignment	not modelled	30.0	20	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
40	c2gb5B_	Alignment	not modelled	25.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
41	c1s1i9_	Alignment	not modelled	25.1	20	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**60s ribosomal protein l43; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
42	c3ndjA_	Alignment	not modelled	24.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
43	d1dl6a_	Alignment	not modelled	23.8	14	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
44	d1g47a1	Alignment	not modelled	22.2	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
45	c3jyw9_	Alignment	not modelled	19.3	18	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**60s ribosomal protein l43; **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
46	d2k4xa1	Alignment	not modelled	19.0	29	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27a
47	d1ctla1	Alignment	not modelled	18.3	20	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
48	d1qxfa_	Alignment	not modelled	15.7	30	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27e
49	d2i9be3	Alignment	not modelled	15.5	14	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Extracellular domain of cell surface receptors
50	d2fd6u3	Alignment	not modelled	15.4	36	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Extracellular domain of cell surface receptors
51	c2f9iD_	Alignment	not modelled	14.8	26	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
52	d2baia1	Alignment	not modelled	14.6	57	**Fold:**Viral leader polypeptide zinc finger **Superfamily:**Viral leader polypeptide zinc finger **Family:**Viral leader polypeptide zinc finger
53	c2jvyA_	Alignment	not modelled	14.5	63	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** solution structure of the eda-id-related c417f mutant of2 human nemo zinc finger
54	c2js4A_	Alignment	not modelled	14.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein bb2007; **PDBTitle:** solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3

						bor54
55	d1ee8a3	Alignment	not modelled	13.6	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
56	d2ctda1	Alignment	not modelled	13.2	63	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
57	c3gn5B_	Alignment	not modelled	13.1	29	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator mqsa (ygit/b3021); **PDBTitle:** structure of the e. coli protein mqsa (ygit/b3021)
58	c2opfA_	Alignment	not modelled	13.0	20	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
59	d1hdoa_	Alignment	not modelled	13.0	50	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
60	d1twfi1	Alignment	not modelled	12.9	27	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
61	c3iz6X_	Alignment	not modelled	12.9	18	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**40s ribosomal protein s27 (s27e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
62	d1r2za3	Alignment	not modelled	12.7	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
63	d5gata_	Alignment	not modelled	12.5	30	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
64	d1k82a3	Alignment	not modelled	12.4	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
65	c2aklA_	Alignment	not modelled	12.1	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phna-like protein pa0128; **PDBTitle:** solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
66	d1osxa_	Alignment	not modelled	11.9	57	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**BAFF receptor-like
67	c2jr6A_	Alignment	not modelled	11.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein nma0874; **PDBTitle:** solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
68	d1dxsa_	Alignment	not modelled	11.8	50	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
69	d1hk8a_	Alignment	not modelled	11.6	35	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
70	c1hk8A_	Alignment	not modelled	11.6	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
71	c1p0tq_	Alignment	not modelled	11.5	57	**PDB header:**protein binding **Chain:** Q: **PDB Molecule:**tumor necrosis factor receptor superfamily **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
72	d1weva_	Alignment	not modelled	11.5	23	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**PHD domain
73	d1oqen_	Alignment	not modelled	11.4	57	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**BAFF receptor-like
74	d1l1ta3	Alignment	not modelled	11.2	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
75	c2pq1B_	Alignment	not modelled	11.1	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ap4a hydrolase; **PDBTitle:** crystal structure of ap4a hydrolase complexed with amp and2 atp (aq_158) from aquifex aeolicus vf5
76	c2jneA_	Alignment	not modelled	10.8	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein yfgj; **PDBTitle:** nmr structure of e.coli yfgj modelled with two zn+2 bound.2 northeast structural genomics consortium target er317.
77	d2jnea1	Alignment	not modelled	10.8	30	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
78	c3lpeF_	Alignment	not modelled	10.8	29	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
79	c1cl4A_	Alignment	not modelled	10.6	50	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (gag polyprotein); **PDBTitle:** nucleocapsid protein from mason-pfizer monkey virus (mpmv)
						Fold: Rubredoxin-like

80	d2akla2	Alignment	not modelled	10.5	26	**Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
81	d1ffya1	Alignment	not modelled	10.1	57	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
82	c3a44D_	Alignment	not modelled	10.0	42	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
83	d1tdza3	Alignment	not modelled	9.9	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
84	d1ryqa_	Alignment	not modelled	9.9	15	**Fold:**Rubredoxin-like **Superfamily:**RNA polymerase subunits **Family:**RpoE2-like
85	d2cu8a1	Alignment	not modelled	9.8	67	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
86	c2f5qA_	Alignment	not modelled	9.7	18	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
87	c2gajA_	Alignment	not modelled	9.7	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
88	c2kwjA_	Alignment	not modelled	9.7	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**zinc finger protein dpf3; **PDBTitle:** solution structures of the double phd fingers of human transcriptional2 protein dpf3 bound to a histone peptide containing acetylation at3 lysine 14
89	c2kdxA_	Alignment	not modelled	9.6	15	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
90	c3mjhD_	Alignment	not modelled	9.5	57	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**early endosome antigen 1; **PDBTitle:** crystal structure of human rab5a in complex with the c2h2 zinc finger2 of eea1
91	d1oqek_	Alignment	not modelled	9.4	35	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**BAFF receptor-like
92	c2xzm6_	Alignment	not modelled	9.3	24	**PDB header:**ribosome **Chain:** 6: **PDB Molecule:**rps27e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
93	d1pvma3	Alignment	not modelled	9.2	23	**Fold:**Rubredoxin-like **Superfamily:**Hypothetical protein Ta0289 C-terminal domain **Family:**Hypothetical protein Ta0289 C-terminal domain
94	c2f9yB_	Alignment	not modelled	9.1	32	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl transferase subunit **PDBTitle:** the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
95	d2f9yb1	Alignment	not modelled	9.1	32	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
96	d1vd4a_	Alignment	not modelled	9.1	56	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
97	d1imla1	Alignment	not modelled	9.0	67	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
98	d2gmga1	Alignment	not modelled	9.0	40	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
99	c2bx9J_	Alignment	not modelled	9.0	38	**PDB header:**transcription regulation **Chain:** J: **PDB Molecule:**tryptophan rna-binding attenuator protein-inhibitory **PDBTitle:** crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions